Table 2.--continued

| Chromosome III | Port Moresby Range % | Bulolo Range % |
|---|---|---|
| Standard | 52.9 - 72.2 | 27.1 - 28.6 |
| A | 2.3 - 5.6 | 0 - 0.9 |
| B | 1.0 - 6.7 | 0 - 0.9 |
| D | 4.4 - 9.8 | 45.8 - 53.5 |
| E | 22.2 - 41.3 | 49.6 - 54.8 |
| H | 0 - 1.5 | 12.2 - 13.4 |
| I | 0 - 1.1 | 14.6 - 21.6 |
| J | - | 0 - 0.3 |
| Flies scored | 361 | 476 |

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References: Mather, W. B., 1961. Chromosomal polymorphism in Drosophila rubida Mather Genetics, 46, 797.

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McIntire, Sarah A. and Thomas Gregg. Miami University, Oxford, Ohio. Pteridines and the white locus in D. melanogaster.

It has been shown by Green (Heredity, 1959) and Judd (Genetics, 1964) that the white locus in D. melanogaster is genetically complex in that non-complementary mutations exist in at least five different sites that are separable by crossing over. It has also been shown (Gregg unpublished) that, to some extent, different alleles at the white locus control the presence of different pteridine compounds associated with red pigment in the wild type eye. Since the pteridines are a more direct reflection of the action of the genes that control their presence than the phenotype of the eye itself, it was felt that a study of the pteridines present in heads of mutant individuals carrying different white alleles might clarify the nature of the genetic complexity of the locus.

Pteridine accumulation patterns for thirty-seven white alleles were determined, using chromatographic methods similar to those of Throckmorton (Univ. Texas Publ. 6205), but using a paper in the shape of an Erlenmeyer flask silhouette (Harrison, Hayes, and Chua, Ohio Jour. Sci. in press) for better separation. The results are shown in the table below.

It appears to be impossible to explain the ten patterns in terms of a single genetic block, which would indicate that the locus is polycistronic in nature. But, if the white locus is polycistronic and if the established recombination sites represent different cistrons, it is surprising to find mutations at different sites producing the same pattern of pteridine accumulation. This particular observation is more readily explained if one assumes that the white locus is a single cistron. It is also difficult to explain the results by assuming that there are several cistrons present, any one of which could contain more than one of the established recombination sites. For instance, if pattern II is controlled by a cistron containing sites 1, 2, and 4, then it should also contain 3, but alleles at 3 produce at least two other patterns, III and IV, but not pattern II. The same is true for pattern IV, in that this pattern is produced by alleles at sites 2, 3, and 5, while alleles at site 4 produce other patterns.

However, the difficulties of explaining the lack of correspondence between the recombination sites and the pteridine patterns, assuming a polycistronic locus, appear to be considerably less troublesome than explaining the ten different patterns on the basis of a locus containing a single cistron. Therefore, in spite of the lack of correspondence, the existence of ten distinct patterns appears to be strong evidence for the polycistronic nature of the white locus.

Table 1.--Pteridine Accumulations Controlled by Various Alleles at the White Locus

| | + aRM A58K11 a58112 mR7aH1 $m^4$ $m^4w$ r,dup | Bwx 1* bf 2 $bf^2$ e 4 $e^2$ 4 ch 4 | sat 2 crr a 3 $a^2$ 3 $a^4$ 3 | col 2 sp-w 5 sp $sp\text{-}w^4$ $a^3$ 3 co 3 | bl | cf cp | i h 4 "a"59e15 | w 4 17G2 57 r,def t | 11E4 | $ec^3$ |
|---|---|---|---|---|---|---|---|---|---|---|
| Drosopterins | ++++ | - | (+) | (+) | - | ++ | - | - | (+) | + |
| Isoxanthopterin | +++ | (+) | + | (+) | + | + | - | - | - | - |
| Xanthopterin | +++ | - | (+) | + | + | (+) | - | - | - | - |
| Blue-violet | ++ | - | - | - | (+) | - | - | - | - | - |
| Sepiapteridine | ++ | (+) | ++ | +++ | (+) | ++ | - | - | - | - |
| 2-amino-4-hydroxypteridine | +++ | - | - | - | - | - | - | - | - | (+) |
| Biopterin | +++ | (+) | ++ | +++ | +++ | ++ | (+) | - | - | - |
| | I | II | III | IV | V | VI | VII | VIII | IX | X |

*Recombination site (Judd, Genetics, 1964)

++++ very large amount
+++ large amount
++ moderate amount
+ small amount
(+) trace amount
- none

Ritossa, F. M. and P. Cammarano. Oak Ridge National Laboratory, Tenn. Isolation and properties of ribosomes from D. melanogaster.

D. melanogaster larvae were homogenized in an all-glass apparatus with two volumes of a medium containing 0.05M Tris pH 7.6, 0.025M KCL, 0.005M 2-mercaptoethanol, 0.25M sucrose; when present, $Mg^{++}$ was either 0.1 or 5mM. The homogenate was centrifuged 20 min. at 20,000 x g, and the resulting postmitochondrial supernatant was further centrifuged at 105,000 x g for 90 min. The material sedimenting at 105,000 x g was resuspended in the homogenization medium and immediately used for analysis in a 10%-34% sucrose density gradient. At times, sodium deoxycholate (1.2%) was added to the postmitochondrial supernatant; in this case, the material sedimented at 105,000 x g was resuspended in the above medium and recentrifuged at 105,000 x g for 90 min. Occasionally homogenization was performed by grinding the tissue under liquid nitrogen; the resulting powder was resuspended in the homogenization medium and processed as above. Isolation of the particles in the medium containing 5mM $Mg^{++}$ led to the appearance of a heavy peak of approximately 170 S (fig. 1A). Treatment of the isolated material with amounts of ribonuclease which are known to result in selective breakage of the interribosomal RNA (10 mμg/mg of RNA) in a variety of materials did not alter the sedimentation profile of this peak. The same sedimentation profile was observed when DOC was used during the isolation procedure.

Centrifugation of the same preparations in a sucrose density gradient in the absence of $Mg^{++}$ results in the resolution of a minor protein component uniformly spread throughout the gradient and a sharp peak sedimenting in the region pertaining to particles of sedimentation constant 80-83 (fig. 1A); this peak showed a 280/260 ratio typical of ribonucleoprotein particles (0.54). No evidence existed for the appearance of subunits of the main peak component comparable to the 50 S and 30 S subunits described in other organisms. The extent of these phenomena was not influenced by either changes in the homogenization conditions or by the use